

1644

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/224,556

DATE: 05/01/2000
TIME: 08:19:50

Input Set : A:\templst.txt
Output Set: N:\CRF3\050100\I224556.raw

4 <110> APPLICANT: Dixit, Vishva M.
6 <120> TITLE OF INVENTION: CD40 BINDING COMPOSITIONS AND METHODS OF
7 USING SAME
9 <130> FILE REFERENCE: 128019201702
11 <140> CURRENT APPLICATION NUMBER: 09/224,556
12 <141> CURRENT FILING DATE: 1998-12-30
14 <150> PRIOR APPLICATION NUMBER: 08/826,577
15 <151> PRIOR FILING DATE: 1997-04-02
17 <150> PRIOR APPLICATION NUMBER: 08/404,832
18 <151> PRIOR FILING DATE: 1995-03-13
20 <160> NUMBER OF SEQ ID NOS: 16
22 <170> SOFTWARE: FastSEQ for Windows Version 3.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 2339
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (211)...(1911)
33 <400> SEQUENCE: 1
34 acgaaggcca cgcgccggcg gccctgagc cggccgagcg gcgacggacc gcgagatgag 60
35 gaaaatgagg cccaaagaag tgaaggcact tggtaagggt cccagagcag gtcagaatca 120
36 gacctaggat cagaaacctg gctcctggct cctgctccct actcttctaa ggatcgctgt 180
37 cctgacagaa gagaactcct ctttctctaa atg gag tcg agt aaa aag atg gac 234
38 Met Glu Ser Ser Lys Lys Met Asp
39 1 5
41 tct cct ggc gcg ctg cag act aac ccg ccg cta aag ctg cac act gac 282
42 Ser Pro Gly Ala Leu Gln Thr Asn Pro Pro Leu Lys Leu His Thr Asp
43 10 15 20
45 cgc agt gct ggg acg cca gtt ttt gtc cct gaa caa gga ggt tac aag 330
46 Arg Ser Ala Gly Thr Pro Val Phe Val Pro Glu Gln Gly Gly Tyr Lys
47 25 30 35 40
49 gaa aag ttt gtg aag acc gtg gag gac aag tac aag tgt gag aag tgc 378
50 Glu Lys Phe Val Lys Thr Val Glu Asp Lys Tyr Lys Cys Glu Lys Cys
51 45 50 55
53 cac ctg gtg ctg tgc agc ccg aag cag acc gag tgt ggg cac cgc ttc 426
54 His Leu Val Leu Cys Ser Pro Lys Gln Thr Glu Cys Gly His Arg Phe
55 60 65 70
57 tgc gag agc tgc atg gcg gcc ctg ctg agc tct tca agt cca aaa tgt 474
58 Cys Glu Ser Cys Met Ala Ala Leu Leu Ser Ser Ser Pro Lys Cys
59 75 80 85
61 aca gcg tgt caa gag agc atc gtt aaa gat aag gtg ttt aag gat aat 522
62 Thr Ala Cys Gln Glu Ser Ile Val Lys Asp Lys Val Phe Lys Asp Asn
63 90 95 100
65 tgc tgc aag aga gaa att ctg gct ctt cag atc tat tgt cgg aat gaa 570
66 Cys Cys Lys Arg Glu Ile Leu Ala Leu Gln Ile Tyr Cys Arg Asn Glu
67 105 110 115 120

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69	agc aga ggt tgt gca gag cag tta atg ctg gga cat ctg gtg cat tta	618
70	Ser Arg Gly Cys Ala Glu Gln Leu Met Leu Gly His Leu Val His Leu	
71	125 130 135	
73	aaa aat gat tgc cat ttt gaa gaa ctt cca tgt gtg cgt cct gac tgc	666
74	Lys Asn Asp Cys His Phe Glu Glu Leu Pro Cys Val Arg Pro Asp Cys	
75	140 145 150	
77	aaa gaa aag gtc ttg agg aaa gac ctg cga gac cac gtg gag aag gcg	714
78	Lys Glu Lys Val Leu Arg Lys Asp Leu Arg Asp His Val Glu Lys Ala	
79	155 160 165	
81	tgt aaa tac cgg gaa gcc aca tgc agc cac tgc aag agt cag gtt ccg	762
82	Cys Lys Tyr Arg Glu Ala Thr Cys Ser His Cys Lys Ser Gln Val Pro	
83	170 175 180	
85	atg atc gcg ctg cag aaa cac gaa gac acc gac tgt ccc tgc gtg gtg	810
86	Met Ile Ala Leu Gln Lys His Glu Asp Thr Asp Cys Pro Cys Val Val	
87	185 190 195 200	
89	gtg tcc tgc cct cac aag tgc agc gtc cag act ctc ctg agg agc gag	858
90	Val Ser Cys Pro His Lys Cys Ser Val Gln Thr Leu Leu Arg Ser Glu	
91	205 210 215	
93	ttg agt gca cac ttg tca gag tgt gtc aat gcc ccc agc acc tgt agt	906
94	Leu Ser Ala His Leu Ser Glu Cys Val Asn Ala Pro Ser Thr Cys Ser	
95	220 225 230	
97	ttt aag cgc tat ggc tgc gtt ttt cag ggg aca aac cag cag atc aag	954
98	Phe Lys Arg Tyr Gly Cys Val Phe Gln Gly Thr Asn Gln Ile Lys	
99	235 240 245	
101	gcc cac gag gcc agc tcc gcc gtg cag cac gtc aac ctg ctg aag gag	1002
102	Ala His Glu Ala Ser Ser Ala Val Gln His Val Asn Leu Leu Lys Glu	
103	250 255 260	
105	tgg agc aac tcg ctc gaa aag aag gtt tcc ttg ttg cag aat gaa agt	1050
106	Trp Ser Asn Ser Leu Glu Lys Lys Val Ser Leu Leu Gln Asn Glu Ser	
107	265 270 275 280	
109	gta gaa aaa aac aag agc ata caa agt ttg cac aat cag ata tgt agc	1098
110	Val Glu Lys Asn Lys Ser Ile Gln Ser Leu His Asn Gln Ile Cys Ser	
111	285 290 295	
113	ttt gaa att gaa att gag aga caa aag gaa atg ctt cga aat aat gaa	1146
114	Phe Glu Ile Glu Ile Glu Arg Gln Lys Glu Met Leu Arg Asn Asn Glu	
115	300 305 310	
117	tcc aaa atc ctt cat tta cag cga gtg ata gac agc caa gca gag aaa	1194
118	Ser Lys Ile Leu His Leu Gln Arg Val Ile Asp Ser Gln Ala Glu Lys	
119	315 320 325	
121	ctg aag gag ctt gac aag gag atc cgg ccc ttc cgg cag aac tgg gag	1242
122	Leu Lys Glu Leu Asp Lys Glu Ile Arg Pro Phe Arg Gln Asn Trp Glu	
123	330 335 340	
125	gaa gca gac agc atg aag agc agc gtg gag tcc ctc cag aac cgc gtg	1290
126	Glu Ala Asp Ser Met Lys Ser Ser Val Glu Ser Leu Gln Asn Arg Val	
127	345 350 355 360	
129	acc gag ctg gag agc gtg gac aag agc gcg ggg caa gtg gct cgg aac	1338
130	Thr Glu Leu Glu Ser Val Asp Lys Ser Ala Gly Gln Val Ala Arg Asn	
131	365 370 375	
133	aca ggc ctg ctg gag tcc cag ctg agc cgg cat gac cag atg ctg agt	1386

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134 Thr Gly Leu Leu Glu Ser Gln Leu Ser Arg His Asp Gln Met Leu Ser
135                               380                               385                               390
137 gtg cac gac atc cgc cta gcc gac atg gac ctg ggc ttc cag gtc ctg      1434
138 Val His Asp Ile Arg Leu Ala Asp Met Asp Leu Gly Phe Gln Val Leu
139                               395                               400                               405
141 gag acc gcc agc tac aat gga gtg ctc atc tgg aag att cgc gac tac      1482
142 Glu Thr Ala Ser Tyr Asn Gly Val Leu Ile Trp Lys Ile Arg Asp Tyr
143                               410                               415                               420
145 aag cgg cgg aag cag gag gcc gtc atg ggg aag acc ctg tcc ctt tac      1530
146 Lys Arg Arg Lys Gln Glu Ala Val Met Gly Lys Thr Leu Ser Leu Tyr
147                               425                               430                               435                               440
149 agc cag cct ttc tac act ggt tac ttt ggc tat aag atg tgt gcc agg      1578
150 Ser Gln Pro Phe Tyr Thr Gly Tyr Phe Gly Tyr Lys Met Cys Ala Arg
151                               445                               450                               455
153 gtc tac ctg aac ggg gac ggg atg ggg aag ggg acg cac ttg tcg ctg      1626
154 Val Tyr Leu Asn Gly Asp Gly Met Gly Lys Gly Thr His Leu Ser Leu
155                               460                               465                               470
157 ttt ttt gtc atc atg cgt gga gaa tat gat gcc ctg ctt cct tgg ccg      1674
158 Phe Phe Val Ile Met Arg Gly Glu Tyr Asp Ala Leu Leu Pro Trp Pro
159                               475                               480                               485
161 ttt aag cag aaa gtg aca ctc atg ctg atg gat cag ggg tcc tct cga      1722
162 Phe Lys Gln Lys Val Thr Leu Met Leu Met Asp Gln Gly Ser Ser Arg
163                               490                               495                               500
165 cgt cat ttg gga gat gca ttc aag ccc gac ccc aac agc agc agc ttc      1770
166 Arg His Leu Gly Asp Ala Phe Lys Pro Asp Pro Asn Ser Ser Ser Phe
167                               505                               510                               515                               520
169 aag aag ccc act gga gag atg aat atc gcc tct tct ggc tgc cca gtc ttt      1818
170 Lys Lys Pro Thr Gly Glu Met Asn Ile Ala Ser Gly Cys Pro Val Phe
171                               525                               530                               535
173 gtg gcc caa act gtt cta gaa aat ggg aca tat att aaa gat gat aca      1866
174 Val Ala Gln Thr Val Leu Glu Asn Gly Thr Tyr Ile Lys Asp Asp Thr
175                               540                               545                               550
177 att ttt att aaa gtc ata gtg gat act tcg gat ctg ccc gat ccc      1911
178 Ile Phe Ile Lys Val Ile Val Asp Thr Ser Asp Leu Pro Asp Pro
179                               555                               560                               565
181 tgataagtag ctggggaggt ggatttagca gaaggcaact cctctggggg atttgaaccg      1971
182 gtctgtcttc actgaggtcc tcgcgctcag aaaaggacct tgtgagacgg aggaagcggc      2031
183 agaaggcgga cgcgtgccgg cgggaggagc cacgcgagag cacacctgac acgttttata      2091
184 atagactagc cacacttcac tctgaagaat tatttatcct tcaacaagat aaatattgct      2151
185 gtcagagaag gttttcattt tcatttttaa agatctagtt aattaaggtg gaaaacatat      2211
186 atgctaaaca aaagaaacat gatttttctt ccttaaacctt gaacacccaa aaaacacaca      2271
187 cacacacaca cgtggggata gctggacatg tcagcatggt aagtaaaagg agaatttatg      2331
188 aaatagta                                     2339
190 <210> SEQ ID NO: 2
191 <211> LENGTH: 567
192 <212> TYPE: PRT
193 <213> ORGANISM: Homo sapiens
195 <400> SEQUENCE: 2
196 Met Glu Ser Ser Lys Lys Met Asp Ser Pro Gly Ala Leu Gln Thr Asn

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197	1			5				10				15		
198	Pro	Pro	Leu	Lys	Leu	His	Thr	Asp	Arg	Ser	Ala	Gly	Thr	Pro
199				20					25				30	Val
200	Val	Pro	Glu	Gln	Gly	Gly	Tyr	Lys	Glu	Lys	Phe	Val	Lys	Thr
201			35					40				45		Val
202	Asp	Lys	Tyr	Lys	Cys	Glu	Lys	Cys	His	Leu	Val	Leu	Cys	Ser
203		50				55					60			Pro
204	Gln	Thr	Glu	Cys	Gly	His	Arg	Phe	Cys	Glu	Ser	Cys	Met	Ala
205	65					70				75				80
206	Leu	Ser	Ser	Ser	Ser	Pro	Lys	Cys	Thr	Ala	Cys	Gln	Glu	Ser
207				85						90				Ile
208	Lys	Asp	Lys	Val	Phe	Lys	Asp	Asn	Cys	Cys	Lys	Arg	Glu	Ile
209			100					105					110	Leu
210	Leu	Gln	Ile	Tyr	Cys	Arg	Asn	Glu	Ser	Arg	Gly	Cys	Ala	Gln
211		115						120				125		Leu
212	Met	Leu	Gly	His	Leu	Val	His	Leu	Lys	Asn	Asp	Cys	His	Phe
213		130						135				140		Glu
214	Leu	Pro	Cys	Val	Arg	Pro	Asp	Cys	Lys	Glu	Lys	Val	Leu	Arg
215	145					150					155			Lys
216	Leu	Arg	Asp	His	Val	Glu	Lys	Ala	Cys	Lys	Tyr	Arg	Glu	Ala
217			165					170						Thr
218	Ser	His	Cys	Lys	Ser	Gln	Val	Pro	Met	Ile	Ala	Leu	Gln	Lys
219			180					185					190	His
220	Asp	Thr	Asp	Cys	Pro	Cys	Val	Val	Val	Ser	Cys	Pro	His	Lys
221			195					200				205		Cys
222	Val	Gln	Thr	Leu	Leu	Arg	Ser	Glu	Leu	Ser	Ala	His	Leu	Ser
223		210					215					220		Glu
224	Val	Asn	Ala	Pro	Ser	Thr	Cys	Ser	Phe	Lys	Arg	Tyr	Gly	Cys
225	225					230					235			Val
226	Gln	Gly	Thr	Asn	Gln	Gln	Ile	Lys	Ala	His	Glu	Ala	Ser	Ser
227			245							250				Ala
228	Gln	His	Val	Asn	Leu	Leu	Lys	Glu	Trp	Ser	Asn	Ser	Leu	Glu
229			260						265				270	Lys
230	Val	Ser	Leu	Leu	Gln	Asn	Glu	Ser	Val	Glu	Lys	Asn	Lys	Ser
231		275						280				285		Ile
232	Ser	Leu	His	Asn	Gln	Ile	Cys	Ser	Phe	Glu	Ile	Glu	Ile	Gln
233		290					295					300		Arg
234	Lys	Glu	Met	Leu	Arg	Asn	Asn	Glu	Ser	Lys	Ile	Leu	His	Leu
235	305					310					315			Gln
236	Val	Ile	Asp	Ser	Gln	Ala	Glu	Lys	Leu	Lys	Glu	Leu	Asp	Lys
237			325							330				Glu
238	Arg	Pro	Phe	Arg	Gln	Asn	Trp	Glu	Glu	Ala	Asp	Ser	Met	Lys
239			340						345				350	Ser
240	Val	Glu	Ser	Leu	Gln	Asn	Arg	Val	Thr	Glu	Leu	Glu	Ser	Val
241		355						360				365		Asp
242	Ser	Ala	Gly	Gln	Val	Ala	Arg	Asn	Thr	Gly	Leu	Leu	Glu	Ser
243		370					375					380		Gln
244	Ser	Arg	His	Asp	Gln	Met	Leu	Ser	Val	His	Asp	Ile	Arg	Leu
245	385					390					395			Ala
														Asp
														400

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246 Met Asp Leu Gly Phe Gln Val Leu Glu Thr Ala Ser Tyr Asn Gly Val
247                               405                410                415
248 Leu Ile Trp Lys Ile Arg Asp Tyr Lys Arg Arg Lys Gln Glu Ala Val
249                               420                425                430
250 Met Gly Lys Thr Leu Ser Leu Tyr Ser Gln Pro Phe Tyr Thr Gly Tyr
251                               435                440                445
252 Phe Gly Tyr Lys Met Cys Ala Arg Val Tyr Leu Asn Gly Asp Gly Met
253                               450                455                460
254 Gly Lys Gly Thr His Leu Ser Leu Phe Phe Val Ile Met Arg Gly Glu
255                               465                470                475                480
256 Tyr Asp Ala Leu Leu Pro Trp Pro Phe Lys Gln Lys Val Thr Leu Met
257                               485                490                495
258 Leu Met Asp Gln Gly Ser Ser Arg Arg His Leu Gly Asp Ala Phe Lys
259                               500                505                510
260 Pro Asp Pro Asn Ser Ser Ser Phe Lys Lys Pro Thr Gly Glu Met Asn
261                               515                520                525
262 Ile Ala Ser Gly Cys Pro Val Phe Val Ala Gln Thr Val Leu Glu Asn
263                               530                535                540
264 Gly Thr Tyr Ile Lys Asp Asp Thr Ile Phe Ile Lys Val Ile Val Asp
265                               545                550                555                560
266 Thr Ser Asp Leu Pro Asp Pro
267                               565
269 <210> SEQ ID NO: 3
270 <211> LENGTH: 49
271 <212> TYPE: PRT
272 <213> ORGANISM: Homo sapiens
274 <400> SEQUENCE: 3
275 Asp Lys Tyr Lys Cys Glu Lys Cys His Leu Val Leu Cys Ser Pro Lys
276 1 5 10 15
277 Gln Thr Glu Cys Gly His Arg Phe Cys Glu Ser Cys Met Ala Ala Leu
278 20 25 30
279 Leu Ser Ser Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile Val
280 35 40 45
281 Lys
284 <210> SEQ ID NO: 4
285 <211> LENGTH: 50
286 <212> TYPE: PRT
287 <213> ORGANISM: Homo sapiens
289 <400> SEQUENCE: 4
290 Ala Lys Tyr Leu Cys Ser Ala Cys Lys Asn Ile Leu Arg Arg Pro Phe
291 1 5 10 15
292 Gln Ala Gln Cys Gly His Arg Tyr Cys Ser Phe Cys Leu Thr Ser Ile
293 20 25 30
294 Leu Ser Ser Gly Pro Gln Asn Cys Ala Ala Cys Val Tyr Glu Gly Leu
295 35 40 45
296 Tyr Glu
297 50
299 <210> SEQ ID NO: 5
300 <211> LENGTH: 49

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